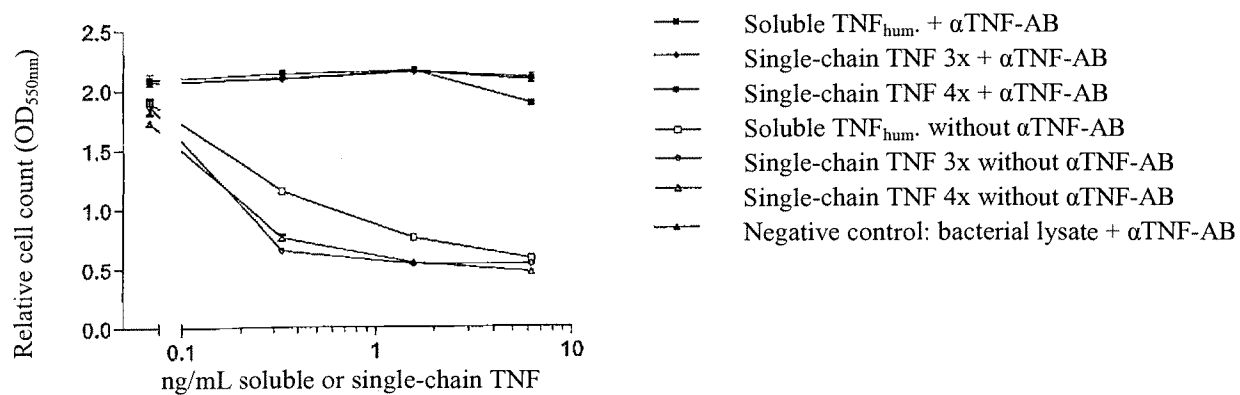


1/41

Cytotoxicity test
sTNF and scTNFs with neutralizing antibodies [AB]

**Figure 1**

2/41

Cytotoxicity test
sTNF and scTNFs on MF-TNFR2

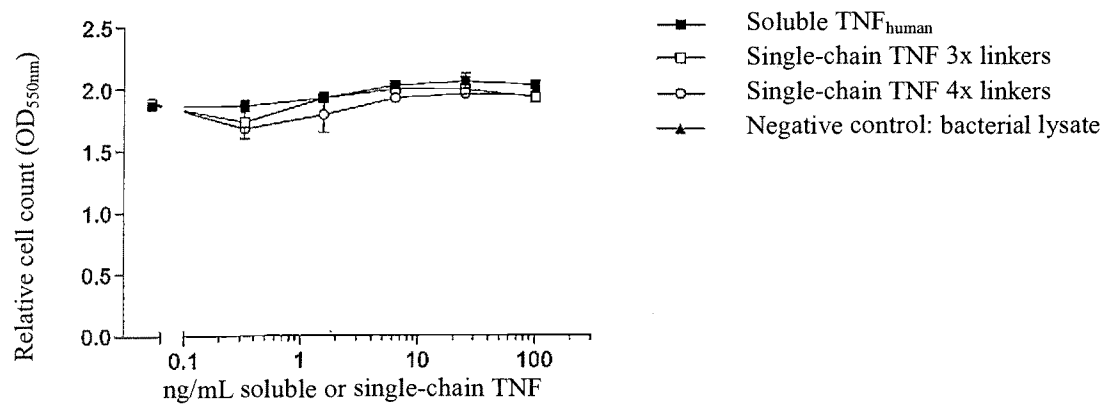
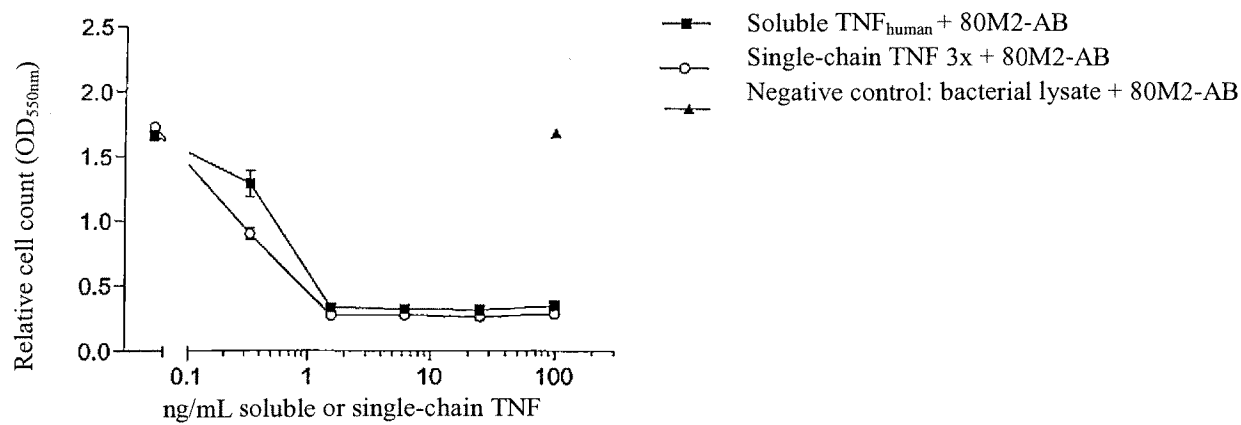


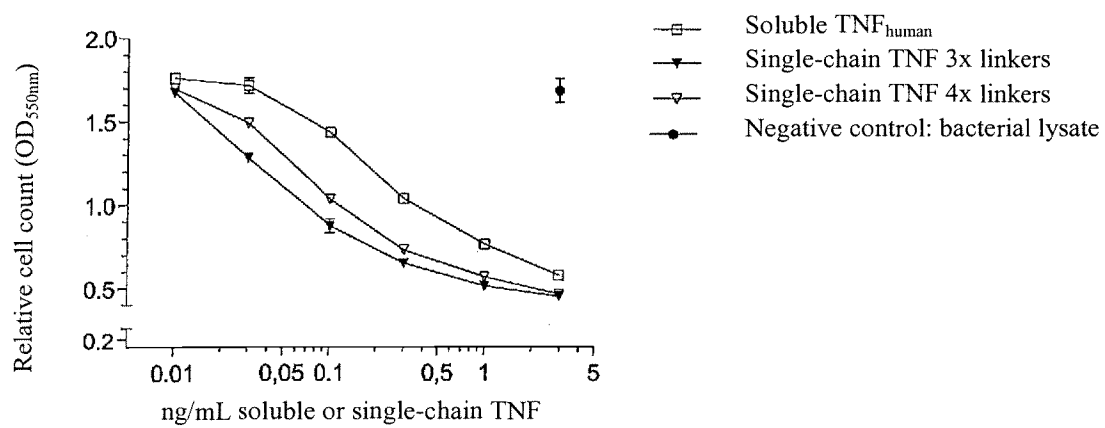
Figure 2

3/41

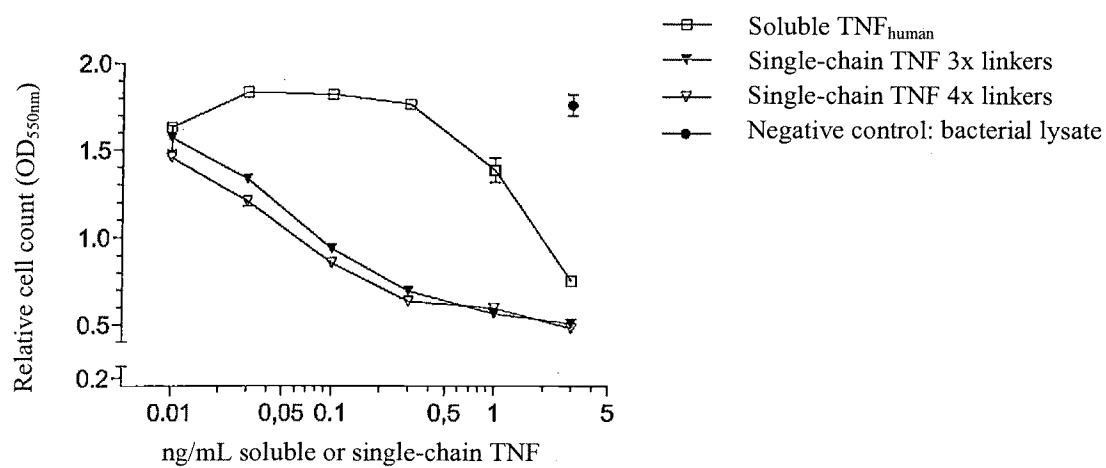
Cytotoxicity test
sTNF and scTNFs on MF-TNFR2 + 80M2

**Figure 3**

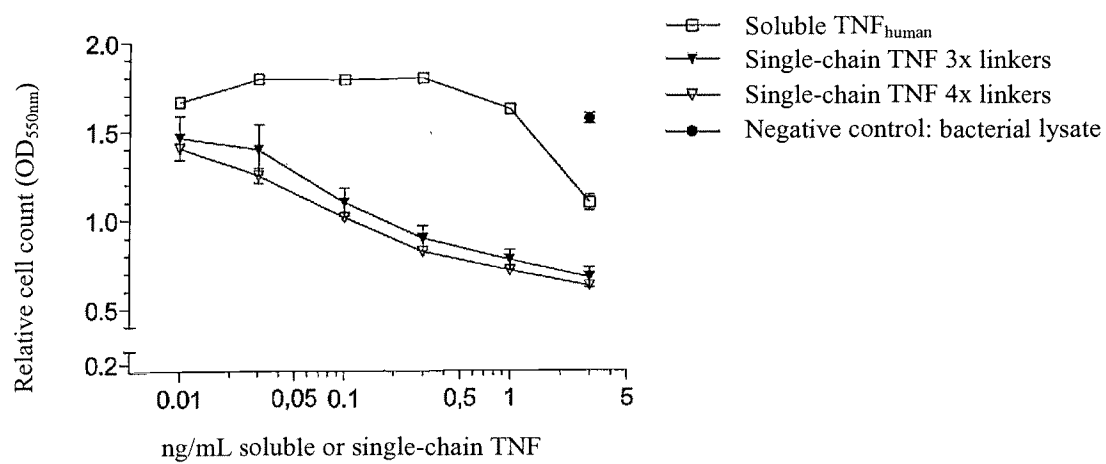
4/41

Stability test with MF – freshly titrated**Figure 4**

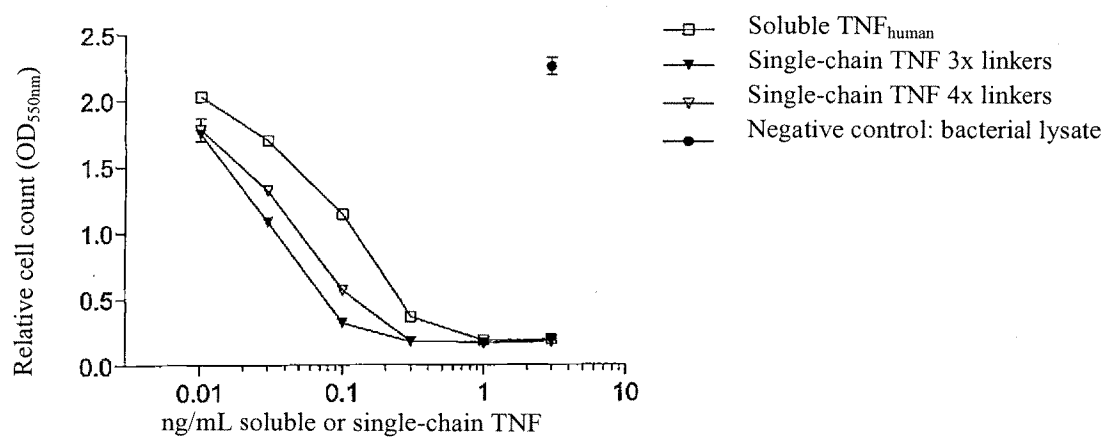
5/41

Stability test with MF – incubated for 8 days**Figure 5**

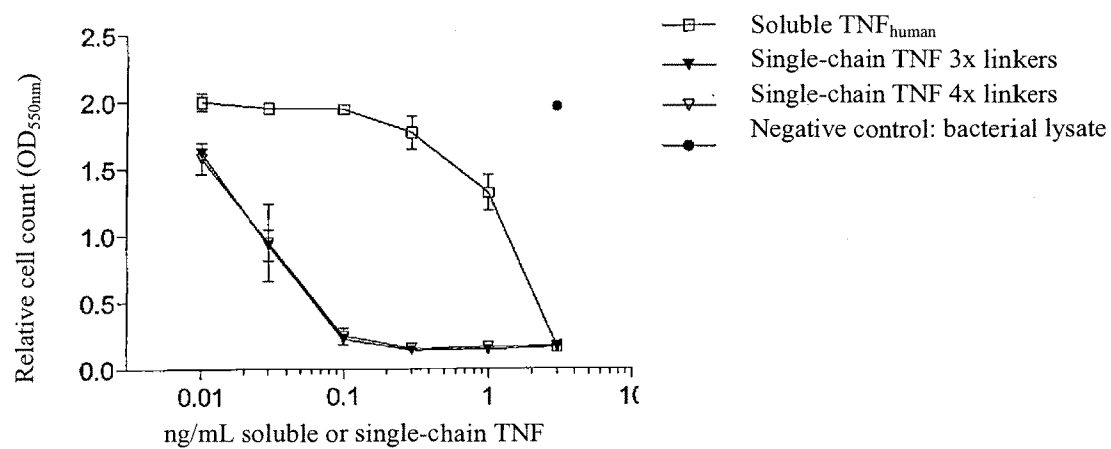
6/41

Stability test with MF – incubated for 14 days**Figure 6**

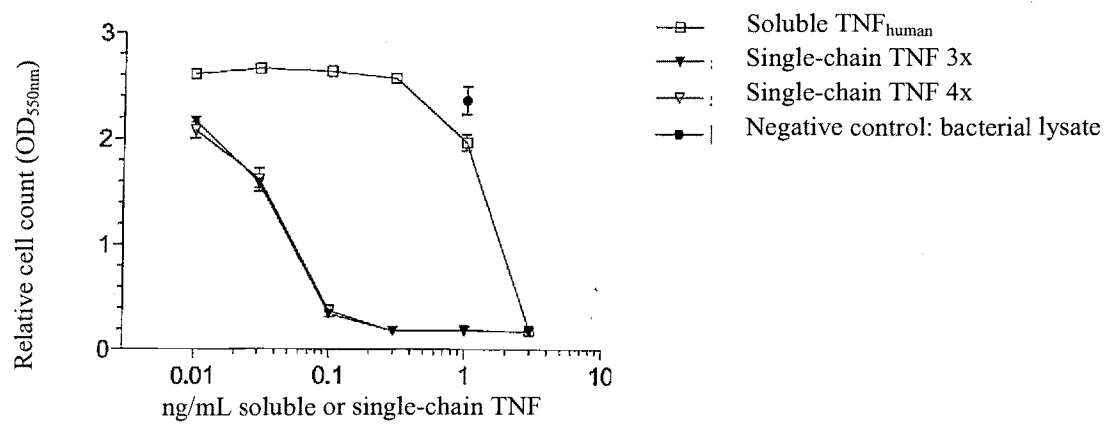
7/41

Stability test with Kym1 – freshly titrated**Figure 7**

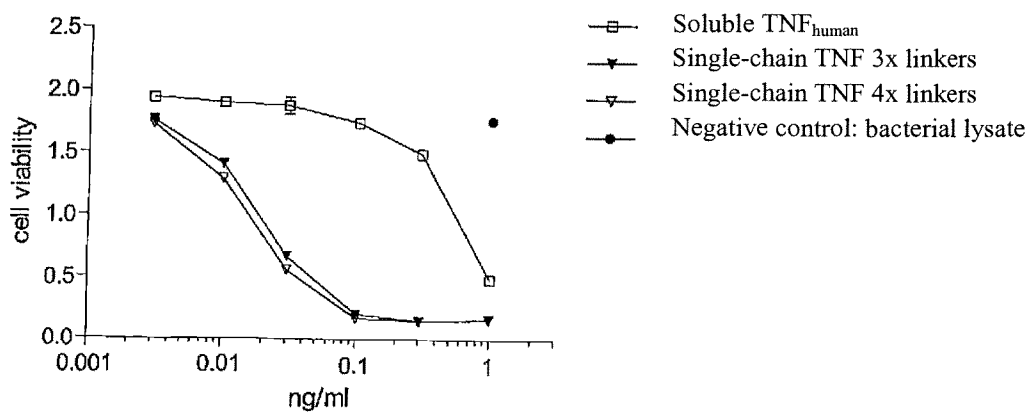
8/41

Stability test with Kym1 – incubated for 16 days**Figure 8**

9/41

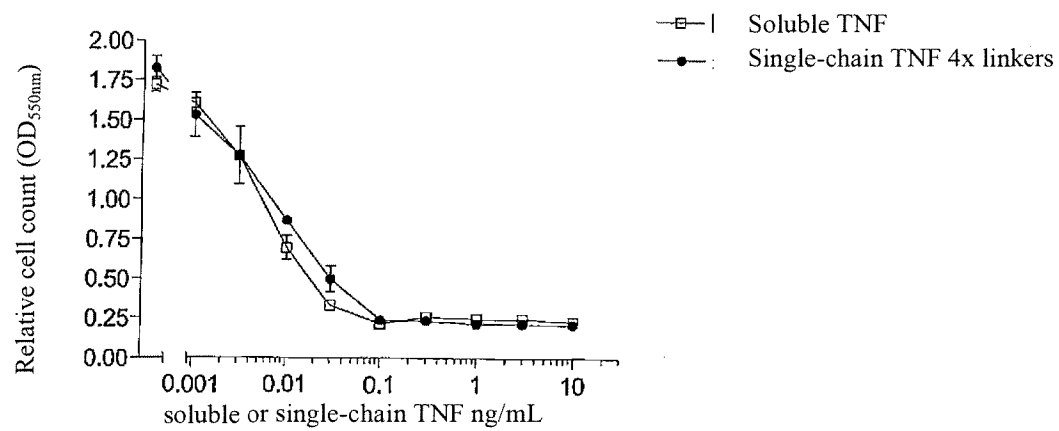
Stability test with Kym1 – incubated for 22 days**Figure 9**

10/41

Stability test with Kym1 – titrated from stock solution**Figure 10**

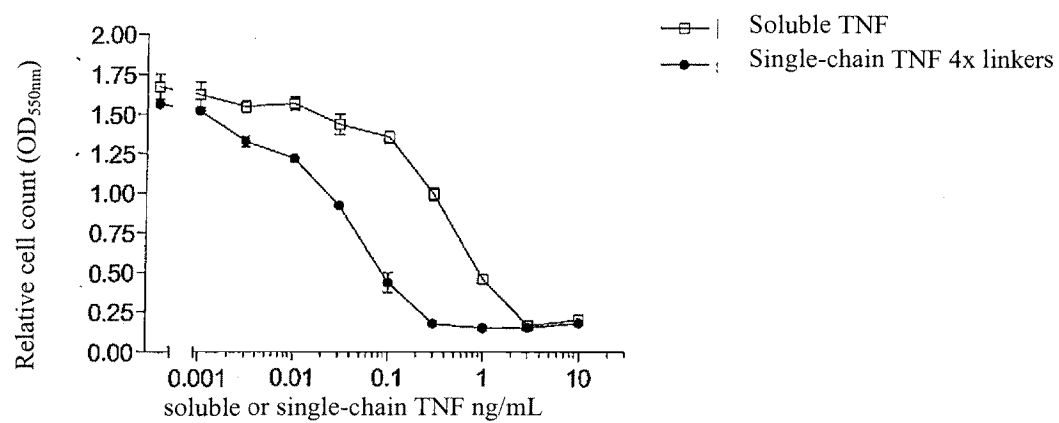
11/41

Stability test with human serum
Serum stability - freshly titrated

**Figure 11**

12/41

Stability test with human serum
Serum stability – 8 days

**Figure 12**

13/41

Silver gel

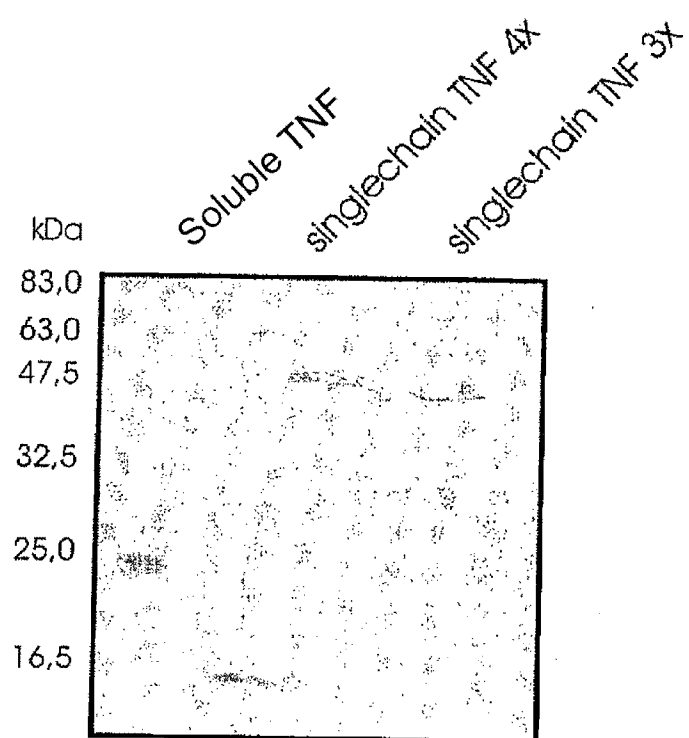


Figure 13

Western Blot

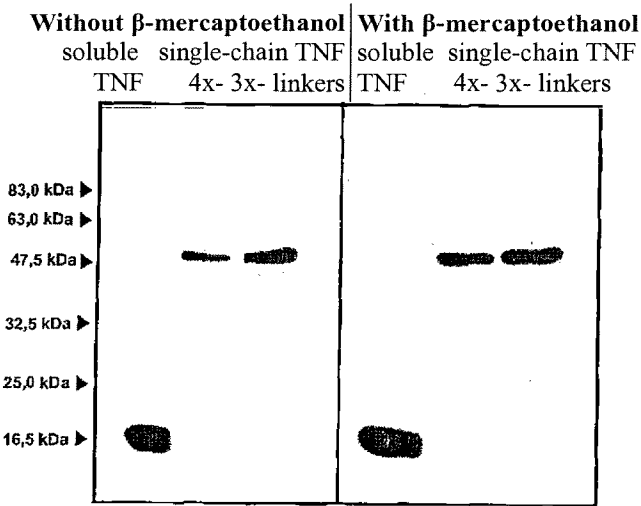
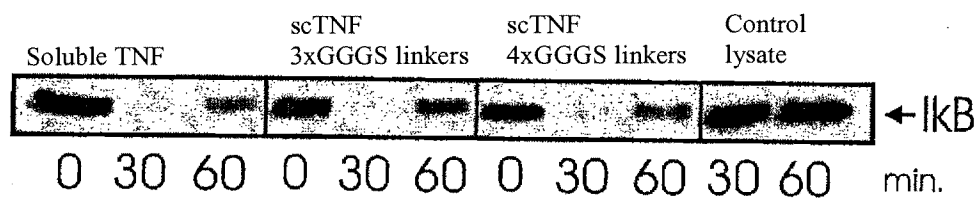
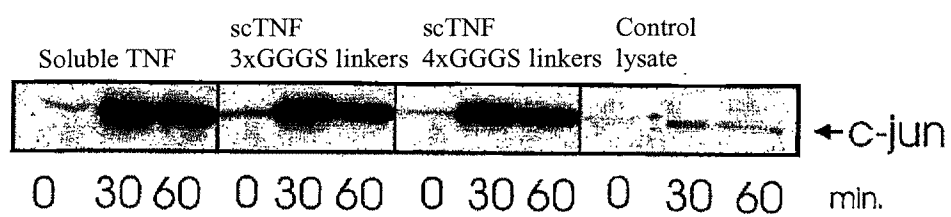


Figure 14

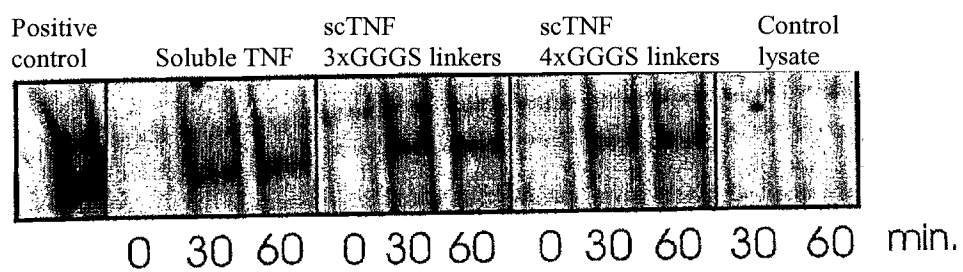
15/41

I κ B degradation assay**Figure 15**

16/41

JNK assay**Figure 16**

17/41

Electrophoretic Mobility Shift Assay (EMSA)**Figure 17**

18/41

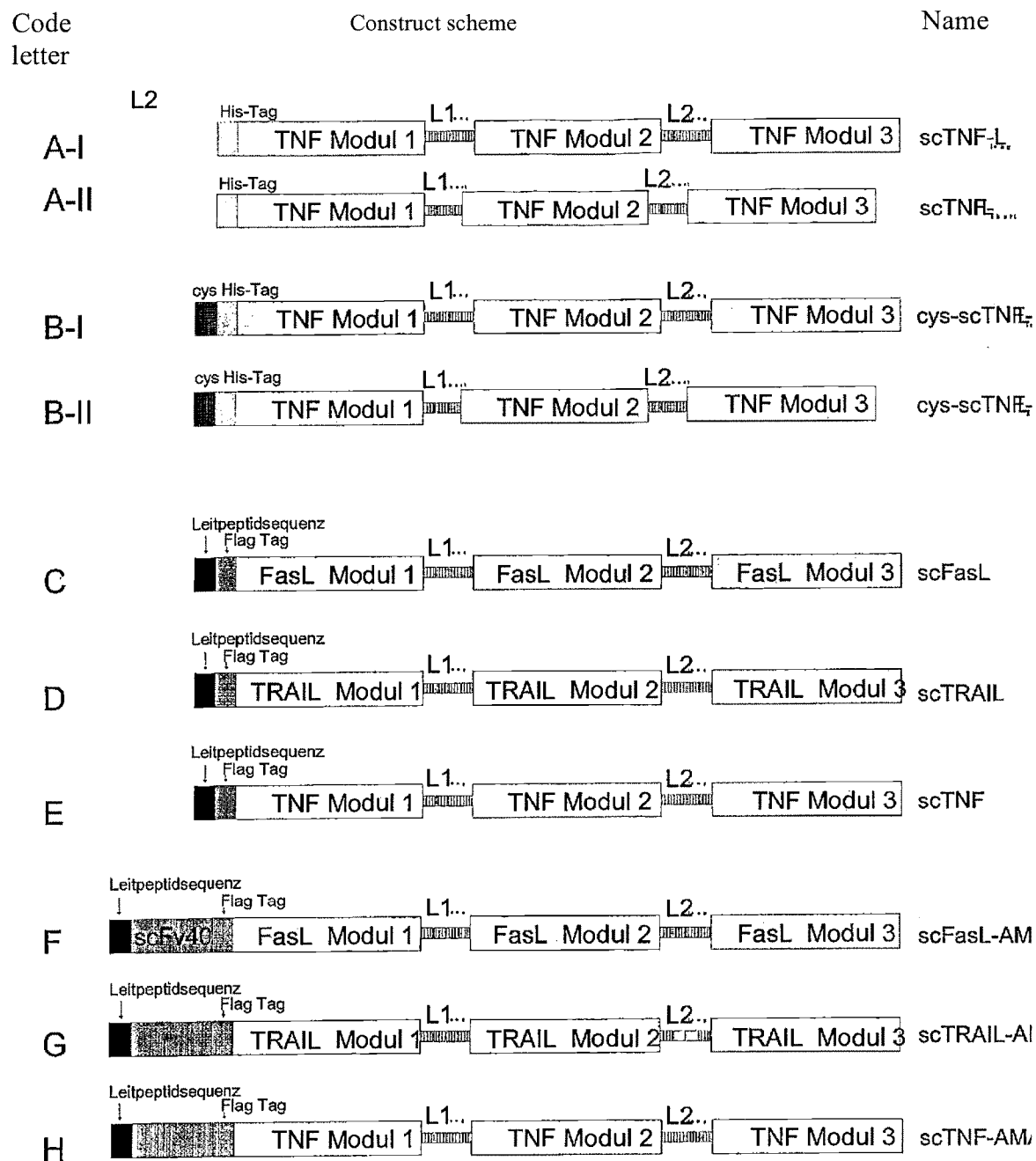


Figure 18

Key: Leitpeptidsequenz = leader peptide sequence
 Modul = module

19/41

Figure 19

Nucleic acid sequence and corresponding amino acid sequence of scTNF-L_{short}
Construct A-II

1	ATG AGA GGA TCG CAT CAC CAT CAC CAT CAC GGA TCA GCG TCG TCT	45
1	M R G S H H H H H H G S A S S	15
46	TCT TCT CGT ACC CCG TCT GAC AAA CCG GTT GCT CAC GTT GTT GCA	90
16	S S R T P S D K P V A H V V A	30
91	AAC CCG CAG GCT GAA GGT CAA CTG CAA TGG CTG AAC CGT CGT GCT	135
31	N P Q A E G Q L Q W L N R R A	45
136	AAC GCT CTG CTG GCT AAC GGT GTT GAA CTG CGT GAC AAC CAG CTG	180
46	N A L L A N G V E L R D N Q L	60
181	GTT GTT CCG TCT GAA GGC CTG TAC CTG ATC TAC TCC CAG GTT CTG	225
61	V V P S E G L Y L I Y S Q V L	75
226	TTC AAA GGC CAG GGC TGC CCG TCC ACC CAC GTT CTG CTG ACC CAC	270
76	F K G Q G C P S T H V L L T H	90
271	ACC ATC TCT CGT ATC GCT GTT TCC TAC CAG ACC AAA GTA AAC CTG	315
91	T I S R I A V S Y Q T K V N L	105
316	CTG TCT GCA ATC AAA TCT CCG TGC CAG CGT GAA ACC CCG GAA GGT	360
106	L S A I K S P C Q R E T P E G	120
361	GCT GAA GCT AAA CCG TGG TAC GAA CCG ATC TAC CTG GGT GGC GTT	405
121	A E A K P W Y E P I Y L G G V	135
406	TTT CAA CTG GAG AAA GGT GAC CGT CTG TCT GCA GAA ATT AAC CGT	450
136	F Q L E K G D R L S A E I N R	150
451	CCG GAC TAC CTG GAC TTC GCA GAA TCT GGT CAG GTT TAC TTC GGT	495
151	P D Y L D F A E S G Q V Y F G	165
496	ATC ATC GCT CTG GGT GGC GGT TCT GGT GGC GGT TCT GGT GGC GGA	540
166	I I A L G G G S G G G S G G G	180
541	TCC TCT TCT CGT ACC CCG TCT GAC AAA CCG GTT GCT CAC GTT GTT	585
181	S S S R T P S D K P V A H V V	195
586	GCA AAC CCG CAG GCT GAA GGT CAA CTG CAA TGG CTG AAC CGT CGT	630
196	A N P Q A E G Q L Q W L N R R	210
631	GCT AAC GCT CTG CTG GCT AAC GGT GTT GAA CTG CGT GAC AAC CAG	675
211	A N A L L A N G V E L R D N Q	225
676	CTG GTT GTT CCG TCT GAA GGC CTG TAC CTG ATC TAC TCC CAG GTT	720
226	L V V P S E G L Y L I Y S Q V	240
721	CTG TTC AAA GGC CAG GGC TGC CCG TCC ACC CAC GTT CTG CTG ACC	765
241	L F K G Q G C P S T H V L L T	255
766	CAC ACC ATC TCT CGT ATC GCT GTT TCC TAC CAG ACC AAA GTA AAC	810
256	H T I S R I A V S Y Q T K V N	270
811	CTG CTG TCT GCA ATC AAA TCT CCG TGC CAG CGT GAA ACC CCG GAA	855
271	L L S A I K S P C Q R E T P E	285

20/41

Continuation of Figure 19

856	GGT GCT GAA GCT AAA CCG TGG TAC GAA CCG ATC TAC CTG GGT GGC	900
286	G A E A K P W Y E P I Y L G G	300
901	GTT TTT CAA CTG GAG AAA GGT GAC CGT CTG TCT GCA GAA ATT AAC	945
301	V F Q L E K G D R L S A E I N	315
946	CGT CCG GAC TAC CTG GAC TTC GCA GAA TCT GGT CAG GTT TAC TTC	990
316	R P D Y L D F A E S G Q V Y F	330
991	GGT ATC ATC GCT CTG GGT GGC GGT TCT GGT GGC GGT TCT GGT GGC	1035
331	G I I A L G G G S G G G S G G	345
1036	GGA TCC TCT TCT CGT ACC CCG TCT GAC AAA CCG GTT GCT CAC GTT	1080
346	G S S S R T P S D K P V A H V	360
1081	GTT GCA AAC CCG CAG GCT GAA GGT CAA CTG CAA TGG CTG AAC CGT	1125
361	V A N P Q A E G Q L Q W L N R	375
1126	CGT GCT AAC GCT CTG CTG GCT AAC GGT GTT GAA CTG CGT GAC AAC	1170
376	R A N A L L A N G V E L R D N	390
1171	CAG CTG GTT GTT CCG TCT GAA GGC CTG TAC CTG ATC TAC TCC CAG	1215
391	Q L V V P S E G L Y L I Y S Q	405
1216	GTT CTG TTC AAA GGC CAG GGC TGC CCG TCC ACC CAC GTT CTG CTG	1260
406	V L F K G Q G C P S T H V L L	420
1261	ACC CAC ACC ATC TCT CGT ATC GCT GTT TCC TAC CAG ACC AAA GTA	1305
421	T H T I S R I A V S Y Q T K V	435
1306	AAC CTG CTG TCT GCA ATC AAA TCT CCG TGC CAG CGT GAA ACC CCG	1350
436	N L L S A I K S P C Q R E T P	450
1351	GAA GGT GCT GAA GCT AAA CCG TGG TAC GAA CCG ATC TAC CTG GGT	1395
451	E G A E A K P W Y E P I Y L G	465
1396	GGC GTT TTT CAA CTG GAG AAA GGT GAC CGT CTG TCT GCA GAA ATT	1440
466	G V F Q L E K G D R L S A E I	480
1441	AAC CGT CCG GAC TAC CTG GAC TTC GCA GAA TCT GGT CAG GTT TAC	1485
481	N R P D Y L D F A E S G Q V Y	495
1486	TTC GGT ATC ATC GCT CTG TGA	1506
496	F G I I A L *	501

21/41

Figure 20

**Nucleic acid sequence and corresponding amino acid sequence of cys-scTNF-L_{short}
Construct B-II**

1	ATG GGA GAG CTC ATC GAA GGT CGC TGC GCC GGT GGA TCT GGT CAT	45
1	M G E L I E G R C A G G S G H	15
46	CAT CAT CAC CAT CAC GGC TCA GAC GGA GCG TCG TCT TCT TCT CGT	90
16	H H H H H G S D G A S S S S R	30
91	ACC CCG TCT GAC AAA CCG GTT GCT CAC GTT GTT GCA AAC CCG CAG	135
31	T P S D K P V A H V V A N P Q	45
136	GCT GAA GGT CAA CTG CAA TGG CTG AAC CGT CGT GCT AAC GCT CTG	180
46	A E G Q L Q W L N R R A N A L	60
181	CTG GCT AAC GGT GTT GAA CTG CGT GAC AAC CAG CTG GTT GTT CCG	225
61	L A N G V E L R D N Q L V V P	75
226	TCT GAA GGC CTG TAC CTG ATC TAC TCC CAG GTT CTG TTC AAA GGC	270
76	S E G L Y L I Y S Q V L F K G	90
271	CAG GGC TGC CCG TCC ACC CAC GTT CTG CTG ACC CAC ACC ATC TCT	315
91	Q G C P S T H V L L T H T I S	105
316	CGT ATC GCT GTT TCC TAC CAG ACC AAA GTA AAC CTG CTG TCT GCA	360
106	R I A V S Y Q T K V N L L S A	120
361	ATC AAA TCT CCG TGC CAG CGT GAA ACC CCG GAA GGT GCT GAA GCT	405
121	I K S P C Q R E T P E G A E A	135
406	AAA CCG TGG TAC GAA CCG ATC TAC CTG GGT GGC GTT TTT CAA CTG	450
136	K P W Y E P I Y L G G V F Q L	150
451	GAG AAA GGT GAC CGT CTG TCT GCA GAA ATT AAC CGT CCG GAC TAC	495
151	E K G D R L S A E I N R P D Y	165
496	CTG GAC TTC GCA GAA TCT GGT CAG GTT TAC TTC GGT ATC ATC GCT	540
166	L D F A E S G Q V Y F G I I A	180
541	CTG GGT GGC GGT TCT GGT GGC GGT TCT GGT GGC GGA TCC TCT TCT	585
181	L G G G S G G G S G G G S S S	195
586	CGT ACC CCG TCT GAC AAA CCG GTT GCT CAC GTT GTT GCA AAC CCG	630
196	R T P S D K P V A H V V A N P	210
631	CAG GCT GAA GGT CAA CTG CAA TGG CTG AAC CGT CGT GCT AAC GCT	675
211	Q A E G Q L Q W L N R R A N A	225
676	CTG CTG GCT AAC GGT GTT GAA CTG CGT GAC AAC CAG CTG GTT GTT	720
226	L L A N G V E L R D N Q L V V	240
721	CCG TCT GAA GGC CTG TAC CTG ATC TAC TCC CAG GTT CTG TTC AAA	765
241	P S E G L Y L I Y S Q V L F K	255
766	GGC CAG GGC TGC CCG TCC ACC CAC GTT CTG CTG ACC CAC ACC ATC	810
256	G Q G C P S T H V L L T H T I	270

Continuation of Figure 20

[illegible]

23/41

Figure 21

Nucleic acid sequence and corresponding amino acid sequence of scFasL**Construct C**

1	ATG GCT ATC ATC TAC CTC ATC CTC CTG TTC ACC GCT GTG CGG GGC	45
1	M A I I Y L I L L F T A V R G	15
46	GCG GCC GCG GAT TAC AAA GAC GAT GAC GAT AAA GAA TTC ACG CGT	90
16	A A A D Y K D D D D K E F T R	30
91	GAA AAA AAG GAG CTG AGG AAA GTG GCC CAT TTA ACA GGC AAG TCC	135
31	E K K E L R K V A H L T G K S	45
136	AAC TCA AGG TCC ATG CCT CTG GAA TGG GAA GAC ACC TAT GGA ATT	180
46	N S R S M P L E W E D T Y G I	60
181	GTC CTG CTT TCT GGA GTG AAG TAT AAG AAG GGT GGC CTT GTG ATC	225
61	V L L S G V K Y K K G G L V I	75
226	AAT GAA ACT GGG CTG TAC TTT GTA TAT TCC AAA GTA TAC TTC CGG	270
76	N E T G L Y F V Y S K V Y F R	90
271	GGT CAA TCT TGC AAC AAC CTG CCC CTG AGC CAC AAG GTC TAC ATG	315
91	G Q S C N N L P L S H K V Y M	105
316	AGG AAC TCT AAG TAT CCC CAG GAT CTG GTG ATG ATG GAG GGG AAG	360
106	R N S K Y P Q D L V M M E G K	120
361	ATG ATG AGC TAC TGC ACT ACT GGG CAG ATG TGG GCC CGC AGC AGC	405
121	M M S Y C T T G Q M W A R S S	135
406	TAC CTG GGG GCA GTG TTC AAT CTT ACC AGT GCT GAT CAT TTA TAT	450
136	Y L G A V F N L T S A D H L Y	150
451	GTC AAC GTA TCT GAG CTC TCT CTG GTC AAT TTT GAG GAA TCT CAG	495
151	V N V S E L S L V N F E E S Q	165
496	ACG TTT TTC GGC TTA TAT AAG CTC GGT GGC GGT TCT GGT GGC GGT	540
166	T F F G L Y K L G G G S G G G	180
541	TCT GGT GGC GGT TCT GGT GGC GGA TCA GAA AAA AAG GAG CTG AGG	585
181	S G G G S G G G S E K K E L R	195
586	AAA GTG GCC CAT TTA ACA GGC AAG TCC AAC TCA AGG TCC ATG CCT	630
196	K V A H L T G K S N S R S M P	210
631	CTG GAA TGG GAA GAC ACC TAT GGA ATT GTC CTG CTT TCT GGA GTG	675
211	L E W E D T Y G I V L L S G V	225
676	AAG TAT AAG AAG GGT GGC CTT GTG ATC AAT GAA ACT GGG CTG TAC	720
226	K Y K K G G L V I N E T G L Y	240
721	TTT GTA TAT TCC AAA GTA TAC TTC CGG GGT CAA TCT TGC AAC AAC	765
241	F V Y S K V Y F R G Q S C N N	255

24/41

Continuation of Figure 21

766	CTG	CCC	CTG	AGC	CAC	AAG	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	CCC	810
256	L	P	L	S	H	K	V	Y	M	R	N	S	K	Y	P	270
811	CAG	GAT	CTG	GTG	ATG	ATG	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	855
271	Q	D	L	V	M	M	E	G	K	M	M	S	Y	C	T	285
856	ACT	GGG	CAG	ATG	TGG	GCC	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	900
286	T	G	Q	M	W	A	R	S	S	Y	L	G	A	V	F	300
901	AAT	CTT	ACC	AGT	GCT	GAT	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	945
301	N	L	T	S	A	D	H	L	Y	V	N	V	S	E	L	315
946	TCT	CTG	GTC	AAT	TTT	GAG	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	990
316	S	L	V	N	F	E	E	S	Q	T	F	F	G	L	Y	330
991	AAG	CTC	GGT	GGC	GGT	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGT	TCT	GGT	1035
331	K	L	G	G	G	S	G	G	G	S	G	G	G	S	G	345
1036	GGC	GGA	TCC	GAA	AAA	AAG	GAG	CTG	AGG	AAA	GTG	GCC	CAT	TTA	ACA	1080
346	G	G	S	E	K	K	E	L	R	K	V	A	H	L	T	360
1081	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	CTG	GAA	TGG	GAA	GAC	ACC	1125
361	G	K	S	N	S	R	S	M	P	L	E	W	E	D	T	375
1126	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	1170
376	Y	G	I	V	L	L	S	G	V	K	Y	K	K	G	G	390
1171	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	TTT	GTA	TAT	TCC	AAA	GTA	1215
391	L	V	I	N	E	T	G	L	Y	F	V	Y	S	K	V	405
1216	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	AAC	CTG	CCC	CTG	AGC	CAC	AAG	1260
406	Y	F	R	G	Q	S	C	N	N	L	P	L	S	H	K	420
1261	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	CCC	CAG	GAT	CTG	GTG	ATG	ATG	1305
421	V	Y	M	R	N	S	K	Y	P	Q	D	L	V	M	M	435
1306	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	ACT	GGG	CAG	ATG	TGG	GCC	1350
436	E	G	K	M	M	S	Y	C	T	T	G	Q	M	W	A	450
1351	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	AAT	CTT	ACC	AGT	GCT	GAT	1395
451	R	S	S	Y	L	G	A	V	F	N	L	T	S	A	D	465
1396	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	TCT	CTG	GTC	AAT	TTT	GAG	1440
466	H	L	Y	V	N	V	S	E	L	S	L	V	N	F	E	480
1441	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	AAG	CTC	TGA				1476
481	E	S	Q	T	F	F	G	L	Y	K	L	*				491

25/41

Figure 22

Nucleic acid sequence and corresponding amino acid sequence of scTRAIL**Construct D**

1	ATG GCT ATC ATC TAC CTC ATC CTC CTG TTC ACC GCT GTG CGG GGC	45
1	M A I I Y L I L L F T A V R G	15
46	GCG GCC GCG GAT TAC AAA GAC GAT GAC GAT AAA GAA TTC GGA ACC	90
16	A A A D Y K D D D D K E F G T	30
91	TCT GAG GAA ACC ATT TCT ACA GTT CAA GAA AAG CAA CAA AAT ATT	135
31	S E E T I S T V Q E K Q Q N I	45
136	TCT CCC CTA GTG AGA GAA AGA GGT CCT CAG AGA GTA GCA GCT CAC	180
46	S P L V R E R G P Q R V A A H	60
181	ATA ACT GGG ACC AGA GGA AGA AGC AAC ACA TTG TCT TCT CCA AAC	225
61	I T G T R G R S N T L S S P N	75
226	TCC AAG AAT GAA AAG GCT CTG GGC CGC AAA ATA AAC TCC TGG GAA	270
76	S K N E K A L G R K I N S W E	90
271	TCA TCA AGG AGT GGG CAT TCA TTC CTG AGC AAC TTG CAC TTG AGG	315
91	S S R S G H S F L S N L H L R	105
316	AAT GGT GAA CTG GTC ATC CAT GAA AAA GGG TTT TAC TAC ATC TAT	360
106	N G E L V I H E K G F Y Y I Y	120
361	TCC CAA ACA TAC TTT CGA TTT CAG GAG GAA ATA AAA GAA AAC ACA	405
121	S Q T Y F R F Q E E I K E N T	135
406	AAG AAC GAC AAA CAA ATG GTC CAA TAT ATT TAC AAA TAC ACA AGT	450
136	K N D K Q M V Q Y I Y K Y T S	150
451	TAT CCT GAC CCT ATA TTG TTG ATG AAA AGT GCT AGA AAT AGT TGT	495
151	Y P D P I L L M K S A R N S C	165
496	TGG TCT AAA GAT GCA GAA TAT GGA CTC TAT TCC ATC TAT CAA GGG	540
166	W S K D A E Y G L Y S I Y Q G	180
541	GGA ATA TTT GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT TCT GTA	585
181	G I F E L K E N D R I F V S V	195
586	ACA AAT GAG CAC TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT TTC	630
196	T N E H L I D M D H E A S F F	210
631	GGG GCC TTT TTA GTT GGC GGT GGC GGT TCT GGT GGC GGT TCT GGT	675
211	G A F L V G G G G S G G G S G	225
676	GGC GGT TCT GGT GGC GGA TCA ACC TCT GAG GAA ACC ATT TCT ACA	720
226	G G S G G G S T S E E T I S T	240
721	GTT CAA GAA AAG CAA CAA AAT ATT TCT CCC CTA GTG AGA GAA AGA	765
241	V Q E K Q Q N I S P L V R E R	255

26/41

Continuation of Figure 22

766	GGT	CCT	CAG	AGA	GTA	GCA	GCT	CAC	ATA	ACT	GGG	ACC	AGA	GGA	AGA	810
256	G	P	Q	R	V	A	A	H	I	T	G	T	R	G	R	270
811	AGC	AAC	ACA	TTG	TCT	TCT	CCA	AAC	TCC	AAG	AAT	GAA	AAG	GCT	CTG	855
271	S	N	T	L	S	S	P	N	S	K	N	E	K	A	L	285
856	GGC	CGC	AAA	ATA	AAC	TCC	TGG	GAA	TCA	TCA	AGG	AGT	GGG	CAT	TCA	900
286	G	R	K	I	N	S	W	E	S	S	R	S	G	H	S	300
901	TTC	CTG	AGC	AAC	TTG	CAC	TTG	AGG	AAT	GGT	GAA	CTG	GTC	ATC	CAT	945
301	F	L	S	N	L	H	L	R	N	G	E	L	V	I	H	315
946	GAA	AAA	GGG	TTT	TAC	TAC	ATC	TAT	TCC	CAA	ACA	TAC	TTT	CGA	TTT	990
316	E	K	G	F	Y	Y	I	Y	S	Q	T	Y	F	R	F	330
991	CAG	GAG	GAA	ATA	AAA	GAA	AAC	ACA	AAG	AAC	GAC	AAA	CAA	ATG	GTC	1035
331	Q	E	E	I	K	E	N	T	K	N	D	K	Q	M	V	345
1036	CAA	TAT	ATT	TAC	AAA	TAC	ACA	AGT	TAT	CCT	GAC	CCT	ATA	TTG	TTG	1080
346	Q	Y	I	Y	K	Y	T	S	Y	P	D	P	I	L	L	360
1081	ATG	AAA	AGT	GCT	AGA	AAT	AGT	TGT	TGG	TCT	AAA	GAT	GCA	GAA	TAT	1125
361	M	K	S	A	R	N	S	C	W	S	K	D	A	E	Y	375
1126	GGA	CTC	TAT	TCC	ATC	TAT	CAA	GGG	GGA	ATA	TTT	GAG	CTT	AAG	GAA	1170
376	G	L	Y	S	I	Y	Q	G	G	I	F	E	L	K	E	390
1171	AAT	GAC	AGA	ATT	TTT	GTT	TCT	GTA	ACA	AAT	GAG	CAC	TTG	ATA	GAC	1215
391	N	D	R	I	F	V	S	V	T	N	E	H	L	I	D	405
1216	ATG	GAC	CAT	GAA	GCC	AGT	TTT	TTC	GGG	GCC	TTT	TTA	GTT	GGC	GGT	1260
406	M	D	H	E	A	S	F	F	G	A	F	L	V	G	G	420
1261	GGC	GGT	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGA	TCC	1305
421	G	G	S	G	G	G	S	G	G	G	S	G	G	G	S	435
1306	ACC	TCT	GAG	GAA	ACC	ATT	TCT	ACA	GTT	CAA	GAA	AAG	CAA	CAA	AAT	1350
436	T	S	E	E	T	I	S	T	V	Q	E	K	Q	Q	N	450
1351	ATT	TCT	CCC	CTA	GTG	AGA	GAA	AGA	GGT	CCT	CAG	AGA	GTA	GCA	GCT	1395
451	I	S	P	L	V	R	E	R	G	P	Q	R	V	A	A	465
1396	CAC	ATA	ACT	GGG	ACC	AGA	GGA	AGA	AGC	AAC	ACA	TTG	TCT	TCT	CCA	1440
466	H	I	T	G	T	R	G	R	S	N	T	L	S	S	P	480
1441	AAC	TCC	AAG	AAT	GAA	AAG	GCT	CTG	GGC	CGC	AAA	ATA	AAC	TCC	TGG	1485
481	N	S	K	N	E	K	A	L	G	R	K	I	N	S	W	495
1486	GAA	TCA	TCA	AGG	AGT	GGG	CAT	TCA	TTC	CTG	AGC	AAC	TTG	CAC	TTG	1530
496	E	S	S	R	S	G	H	S	F	L	S	N	L	H	L	510
1531	AGG	AAT	GGT	GAA	CTG	GTC	ATC	CAT	GAA	AAA	GGG	TTT	TAC	TAC	ATC	1575
511	R	N	G	E	L	V	I	H	E	K	G	F	Y	Y	I	525
1576	TAT	TCC	CAA	ACA	TAC	TTT	CGA	TTT	CAG	GAG	GAA	ATA	AAA	GAA	AAC	1620
526	Y	S	Q	T	Y	F	R	F	Q	E	E	I	K	E	N	540

28/41

Figure 23

Nucleic acid sequence and corresponding amino acid sequence of scTNFConstruct E

1	ATG GCT ATC ATC TAC CTC ATC CTC CTG TTC ACC GCT GTG CGG GGC	45
1	M A I I Y L I L L F T A V R G	15
46	GCG GCC GCG GAT TAC AAA GAC GAT GAC GAT AAA GAA TTC GGA TCA	90
16	A A A D Y K D D D D K E F G S	30
91	TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT GTT GTA GCA	135
31	S S R T P S D K P V A H V V A	45
136	AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC CGG GCC	180
46	N P Q A E G Q L Q W L N R R A	60
181	AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG CTG	225
61	N A L L A N G V E L R D N Q L	75
226	GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	270
76	V V P S E G L Y L I Y S Q V L	90
271	TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC	315
91	F K G Q G C P S T H V L L T H	105
316	ACC ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC	360
106	T I S R I A V S Y Q T K V N L	120
361	CTC TCT GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG	405
121	L S A I K S P C Q R E T P E G	135
406	GCT GAG GCC AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC	450
136	A E A K P W Y E P I Y L G G V	150
451	TTC CAG CTG GAG AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG	495
151	F Q L E K G D R L S A E I N R	165
496	CCC GAC TAT CTC GAC TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG	540
166	P D Y L D F A E S G Q V Y F G	180
541	ATC ATT GCC CTG GGT GGC GGT TCT GGT GGC GGT TCT GGT GGC GGT	585
181	I I A L G G G S G G G S G G S G G	195
586	TCT GGT GGC GGA TCA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT	630
196	S G G G S S S S R T P S D K P	210
631	GTA GCC CAT GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG	675
211	V A H V V A N P Q A E G Q L Q	225
676	TGG CTG AAC CGC CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG	720
226	W L N R R A N A L L A N G V E	240
721	CTG AGA GAT AAC CAG CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC	765
241	L R D N Q L V V P S E G L Y L	255

Continuation of Figure 23

[illegible]

30/41

Figure 24

Nucleic acid sequence and corresponding amino acid sequence of scFasL-AMAIZE Construct F

1	ATG GAC TGG ACC TGG CGC GTG TTT TGC CTG CTC GCC GTG GCT CCT	45
1	M D W T W R V F C L L A V A P	15
46	GGG GCC CAC AGC CAG GTA CAG CTG GTG CAG TCT GGG GGA GGC ATG	90
16	G A H S Q V Q L V Q S G G G M	30
91	GTA GAG CCT GGG GGG TCC CTT AGA CTC TCC TGT GCA GCC TCT GGA	135
31	V E P G G S L R L S C A A S G	45
136	TTC ACT TTC AGT AAT GCC TGG ATG AGC TGG GTC CGC CAG GCT CCA	180
46	F T F S N A W M S W V R Q A P	60
181	GGG AAG GGG CTG GAG TGG GTT GGC CGT ATA AAA AGC AAA GCT GGT	225
61	G K G L E W V G R I K S K A G	75
226	GGT GGG ACA GCA GAG TAC GCT GCA CCC GTG AAA GGC AGA TTC ACC	270
76	G G T A E Y A A P V K G R F T	90
271	ATC TCA AGA GAT GAT TCA CAA AAC ACG CTG TAT CTG CAA ATG AAC	315
91	I S R D D S Q N T L Y L Q M N	105
316	AGC CTG AAA ACC GAC GAC ACA GCC GTG TAT TAC TGT ACC ACA CAT	360
106	S L K T D D T A V Y Y C T T H	120
361	GTC TAC GGT GCC CCC CGG AAC TGG GGC CAG GGA TCC CTG GTC ACC	405
121	V Y G A P R N W G Q G S L V T	135
406	GTC TCC TCA GCC TCC ACC AAG GGC CCA AAG CTT GAA GAA GGT GAA	450
136	V S S A S T K G P K L E E G E	150
451	TTT TCA GAA GCA CGC GTA CAG TCT GTG TTG ACT CAG CCG CCC TCA	495
151	F S E A R V Q S V L T Q P P S	165
496	GTG TCT GCG GCC CCA GGA CAG AAG GTC ACC ATC TCC TGC TCT GGA	540
166	V S A A P G Q K V T I S C S G	180
541	AGC AGC TCC AAC ATT GGA AAT AAT TAT GTC TCC TGG TAC GTT CAA	585
181	S S S N I G N N Y V S W Y V Q	195
586	CTC CCA GGA ACA GCC CCC AAA CTC CTC ATT TAT GAC AAT AAT AAG	630
196	L P G T A P K L L I Y D N N K	210
631	CGA TTC TCA GGA GTT CCT GAC CGA TTC TCT GGC TCC AAG TCT GGC	675
211	R F S G V P D R F S G S K S G	225
676	ACG TCA GCC ACC CTG GGC ATC ACC GGG CTC CAG ACT GGG GAC GAG	720
226	T S A T L G I T G L Q T G D E	240
721	GCC GAT TAT TAC TGC GGA GCA TGG GAT GGC AGC CTG CGT GAA GCG	765
241	A D Y Y C G A W D G S L R E A	255

31/41

Continuation of Figure 24

766	GTA	TTC	GGC	GGA	GGG	ACC	AAG	GTC	ACC	GTC	CTA	GGT	GCG	GCC	GCA	810
256	V	F	G	G	G	T	K	V	T	V	L	G	A	A	A	270
811	GTT	GAG	CTC	GAG	gcg	GCC	GCG	GAT	TAC	AAA	GAC	GAT	GAC	GAT	AAA	855
271	V	E	L	E	A	A	A	D	Y	K	D	D	D	D	K	285
856	GAA	TTC	ACG	CGT	GAA	AAA	AAG	GAG	CTG	AGG	AAA	GTG	GCC	CAT	TTA	900
286	E	F	T	R	E	K	K	E	L	R	K	V	A	H	L	300
901	ACA	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	CTG	GAA	TGG	GAA	GAC	945
301	T	G	K	S	N	S	R	S	M	P	L	E	W	E	D	315
946	ACC	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	990
316	T	Y	G	I	V	L	L	S	G	V	K	Y	K	K	G	330
991	GGC	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	TTT	GTA	TAT	TCC	AAA	1035
331	G	L	V	I	N	E	T	G	L	Y	F	V	Y	S	K	345
1036	GTA	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	AAC	CTG	CCC	CTG	AGC	CAC	1080
346	V	Y	F	R	G	Q	S	C	N	N	L	P	L	S	H	360
1081	AAG	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	CCC	CAG	GAT	CTG	GTG	ATG	1125
361	K	V	Y	M	R	N	S	K	Y	P	Q	D	L	V	M	375
1126	ATG	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	ACT	GGG	CAG	ATG	TGG	1170
376	M	E	G	K	M	M	S	Y	C	T	T	G	Q	M	W	390
1171	GCC	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	AAT	CTT	ACC	AGT	GCT	1215
391	A	R	S	S	Y	L	G	A	V	F	N	L	T	S	A	405
1216	GAT	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	TCT	CTG	GTC	AAT	TTT	1260
406	D	H	L	Y	V	N	V	S	E	L	S	L	V	N	F	420
1261	GAG	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	AAG	CTC	GGT	GGC	GGT	1305
421	E	E	S	Q	T	F	F	G	L	Y	K	L	G	G	G	435
1306	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGA	TCA	GAA	AAA	1350
436	S	G	G	G	S	G	G	G	S	G	G	G	S	E	K	450
1351	AAG	GAG	CTG	AGG	AAA	GTG	GCC	CAT	TTA	ACA	GGC	AAG	TCC	AAC	TCA	1395
451	K	E	L	R	K	V	A	H	L	T	G	K	S	N	S	465
1396	AGG	TCC	ATG	CCT	CTG	GAA	TGG	GAA	GAC	ACC	TAT	GGA	ATT	GTC	CTG	1440
466	R	S	M	P	L	E	W	E	D	T	Y	G	I	V	L	480
1441	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	CTT	GTG	ATC	AAT	GAA	1485
481	L	S	G	V	K	Y	K	K	G	G	L	V	I	N	E	495
1486	ACT	GGG	CTG	TAC	TTT	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAA	1530
496	T	G	L	Y	F	V	Y	S	K	V	Y	F	R	G	Q	510
1531	TCT	TGC	AAC	AAC	CTG	CCC	CTG	AGC	CAC	AAG	GTC	TAC	ATG	AGG	AAC	1575
511	S	C	N	N	L	P	L	S	H	K	V	Y	M	R	N	525
1576	TCT	AAG	TAT	CCC	CAG	GAT	CTG	GTG	ATG	ATG	GAG	GGG	AAG	ATG	ATG	1620
526	S	K	Y	P	Q	D	L	V	M	M	E	G	K	M	M	540

Continuation of Figure 24

[illegible]

33/41

Figure 25

Nucleic acid sequence and corresponding amino acid sequence of scTRAIL-AMAIze

Construct G

1	ATG GAC TGG ACC TGG CGC GTG TTT TGC CTG CTC GCC GTG GCT CCT	45
1	M D W T W R V F C L L A V A P	15
46	GGG GCC CAC AGC CAG GTA CAG CTG GTG CAG TCT GGG GGA GGC ATG	90
16	G A H S Q V Q L V Q S G G G M	30
91	GTA GAG CCT GGG GGG TCC CTT AGA CTC TCC TGT GCA GCC TCT GGA	135
31	V E P G G S L R L S C A A S G	45
136	TTC ACT TTC AGT AAT GCC TGG ATG AGC TGG GTC CGC CAG GCT CCA	180
46	F T F S N A W M S W V R Q A P	60
181	GGG AAG GGG CTG GAG TGG GTT GGC CGT ATA AAA AGC AAA GCT GGT	225
61	G K G L E W V G R I K S K A G	75
226	GGT GGG ACA GCA GAG TAC GCT GCA CCC GTG AAA GGC AGA TTC ACC	270
76	G G T A E Y A A P V K G R F T	90
271	ATC TCA AGA GAT GAT TCA CAA AAC ACG CTG TAT CTG CAA ATG AAC	315
91	I S R D D S Q N T L Y L Q M N	105
316	AGC CTG AAA ACC GAC GAC ACA GCC GTG TAT TAC TGT ACC ACA CAT	360
106	S L K T D D T A V Y Y C T T H	120
361	GTC TAC GGT GCC CCC CGG AAC TGG GGC CAG GGA TCC CTG GTC ACC	405
121	V Y G A P R N W G Q G S L V T	135
406	GTC TCC TCA GCC TCC ACC AAG GGC CCA AAG CTT GAA GAA GGT GAA	450
136	V S S A S T K G P K L E E G E	150
451	TTT TCA GAA GCA CGC GTA CAG TCT GTG TTG ACT CAG CCG CCC TCA	495
151	F S E A R V Q S V L T Q P P S	165
496	GTG TCT GCG GCC CCA GGA CAG AAG GTC ACC ATC TCC TGC TCT GGA	540
166	V S A A P G Q K V T I S C S G	180
541	AGC AGC TCC AAC ATT GGA AAT AAT TAT GTC TCC TGG TAC GTT CAA	585
181	S S S N I G N N Y V S W Y V Q	195
586	CTC CCA GGA ACA GCC CCC AAA CTC CTC ATT TAT GAC AAT AAT AAG	630
196	L P G T A P K L L I Y D N N K	210
631	CGA TTC TCA GGA GTT CCT GAC CGA TTC TCT GGC TCC AAG TCT GGC	675
211	R F S G V P D R F S G S K S G	225
676	ACG TCA GCC ACC CTG GGC ATC ACC GGG CTC CAG ACT GGG GAC GAG	720
226	T S A T L G I T G L Q T G D E	240

34/41

Continuation of Figure 25

721	GCC	GAT	TAT	TAC	TGC	GGA	GCA	TGG	GAT	GGC	AGC	CTG	CGT	GAA	GCG	765
241	A	D	Y	Y	C	G	A	W	D	G	S	L	R	E	A	255
766	GTA	TTC	GGC	GGA	GGG	ACC	AAG	GTC	ACC	GTC	CTA	GGT	GCG	GCC	GCA	810
256	V	F	G	G	G	T	K	V	T	V	L	G	A	A	A	270
811	GTT	GAG	CTC	GAG	GCG	GCC	GCG	GAT	TAC	AAA	GAC	GAT	GAC	GAT	AAA	855
271	V	E	L	E	A	A	A	D	Y	K	D	D	D	D	K	285
856	GAA	TTC	GGA	ACC	TCT	GAG	GAA	ACC	ATT	TCT	ACA	GTT	CAA	GAA	AAG	900
286	E	F	G	T	S	E	E	T	I	S	T	V	Q	E	K	300
901	CAA	CAA	AAT	ATT	TCT	CCC	CTA	GTG	AGA	GAA	AGA	GGT	CCT	CAG	AGA	945
301	Q	Q	N	I	S	P	L	V	R	E	R	G	P	Q	R	315
946	GTA	GCA	GCT	CAC	ATA	ACT	GGG	ACC	AGA	GGA	AGA	AGC	AAC	ACA	TTG	990
316	V	A	A	H	I	T	G	T	R	G	R	S	N	T	L	330
991	TCT	TCT	CCA	AAC	TCC	AAG	AAT	GAA	AAG	GCT	CTG	GGC	CGC	AAA	ATA	1035
331	S	S	P	N	S	K	N	E	K	A	L	G	R	K	I	345
1036	AAC	TCC	TGG	GAA	TCA	TCA	AGG	AGT	GGG	CAT	TCA	TTC	CTG	AGC	AAC	1080
346	N	S	W	E	S	S	R	S	G	H	S	F	L	S	N	360
1081	TTG	CAC	TTG	AGG	AAT	GGT	GAA	CTG	GTC	ATC	CAT	GAA	AAA	GGG	TTT	1125
361	L	H	L	R	N	G	E	L	V	I	H	E	K	G	F	375
1126	TAC	TAC	ATC	TAT	TCC	CAA	ACA	TAC	TTT	CGA	TTT	CAG	GAG	GAA	ATA	1170
376	Y	Y	I	Y	S	Q	T	Y	F	R	F	Q	E	E	I	390
1171	AAA	GAA	AAC	ACA	AAG	AAC	GAC	AAA	CAA	ATG	GTC	CAA	TAT	ATT	TAC	1215
391	K	E	N	T	K	N	D	K	Q	M	V	Q	Y	I	Y	405
1216	AAA	TAC	ACA	AGT	TAT	CCT	GAC	CCT	ATA	TTG	TTG	ATG	AAA	AGT	GCT	1260
406	K	Y	T	S	Y	P	D	P	I	L	L	M	K	S	A	420
1261	AGA	AAT	AGT	TGT	TGG	TCT	AAA	GAT	GCA	GAA	TAT	GGA	CTC	TAT	TCC	1305
421	R	N	S	C	W	S	K	D	A	E	Y	G	L	Y	S	435
1306	ATC	TAT	CAA	GGG	GGA	ATA	TTT	GAG	CTT	AAG	GAA	AAT	GAC	AGA	ATT	1350
436	I	Y	Q	G	G	I	F	E	L	K	E	N	D	R	I	450
1351	TTT	GTT	TCT	GTA	ACA	AAT	GAG	CAC	TTG	ATA	GAC	ATG	GAC	CAT	GAA	1395
451	F	V	S	V	T	N	E	H	L	I	D	M	D	H	E	465
1396	GCC	AGT	TTT	TTC	GGG	GCC	TTT	TTA	GTT	GGC	GGT	GGC	GGT	TCT	GGT	1440
466	A	S	F	F	G	A	F	L	V	G	G	G	G	S	G	480
1441	GGC	GGT	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGA	TCA	ACC	TCT	GAG	GAA	1485
481	G	G	S	G	G	G	S	G	G	G	S	T	S	E	E	495
1486	ACC	ATT	TCT	ACA	GTT	CAA	GAA	AAG	CAA	CAA	AAT	ATT	TCT	CCC	CTA	1530
496	T	I	S	T	V	Q	E	K	Q	Q	N	I	S	P	L	510
1531	GTG	AGA	GAA	AGA	GGT	CCT	CAG	AGA	GTA	GCA	GCT	CAC	ATA	ACT	GGG	1575
511	V	R	E	R	G	P	Q	R	V	A	A	H	I	T	G	525

35/41

Continuation of Figure 25

1576	ACC AGA GGA AGA AGC AAC ACA TTG TCT TCT CCA AAC TCC AAG AAT	1620
526	T R G R S N T L S S P N S K N	540
1621	GAA AAG GCT CTG GGC CGC AAA ATA AAC TCC TGG GAA TCA TCA AGG	1665
541	E K A L G R K I N S W E S S R	555
1666	AGT GGG CAT TCA TTC CTG AGC AAC TTG CAC TTG AGG AAT GGT GAA	1710
556	S G H S F L S N L H L R N G E	570
1711	CTG GTC ATC CAT GAA AAA GGG TTT TAC TAC ATC TAT TCC CAA ACA	1755
571	L V I H E K G F Y Y I Y S Q T	585
1756	TAC TTT CGA TTT CAG GAG GAA ATA AAA GAA AAC ACA AAG AAC GAC	1800
586	Y F R F Q E E I K E N T K N D	600
1801	AAA CAA ATG GTC CAA TAT ATT TAC AAA TAC ACA AGT TAT CCT GAC	1845
601	K Q M V Q Y I Y K Y T S Y P D	615
1846	CCT ATA TTG TTG ATG AAA AGT GCT AGA AAT AGT TGT TGG TCT AAA	1890
616	P I L L M K S A R N S C W S K	630
1891	GAT GCA GAA TAT GGA CTC TAT TCC ATC TAT CAA GGG GGA ATA TTT	1935
631	D A E Y G L Y S I Y Q G G I F	645
1936	GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT TCT GTA ACA AAT GAG	1980
646	E L K E N D R I F V S V T N E	660
1981	CAC TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT TTC GGG GCC TTT	2025
661	H L I D M D H E A S F F G A F	675
2026	TTA GTT GGC GGT GGC GGT TCT GGT GGC GGT TCT GGT GGC GGT TCT	2070
676	L V G G G G S G G G S G G G S	690
2071	GGT GGC GGA TCC ACC TCT GAG GAA ACC ATT TCT ACA GTT CAA GAA	2115
691	G G G S T S E E T I S T V Q E	705
2116	AAG CAA CAA AAT ATT TCT CCC CTA GTG AGA GAA AGA GGT CCT CAG	2160
706	K Q Q N I S P L V R E R G P Q	720
2161	AGA GTA GCA GCT CAC ATA ACT GGG ACC AGA GGA AGA AGC AAC ACA	2205
721	R V A A H I T G T R G R S N T	735
2206	TTG TCT TCT CCA AAC TCC AAG AAT GAA AAG GCT CTG GGC CGC AAA	2250
736	L S S P N S K N E K A L G R K	750
2251	ATA AAC TCC TGG GAA TCA TCA AGG AGT GGG CAT TCA TTC CTG AGC	2295
751	I N S W E S S R S G H S F L S	765
2296	AAC TTG CAC TTG AGG AAT GGT GAA CTG GTC ATC CAT GAA AAA GGG	2340
766	N L H L R N G E L V I H E K G	780
2341	TTT TAC TAC ATC TAT TCC CAA ACA TAC TTT CGA TTT CAG GAG GAA	2385
781	F Y Y I Y S Q T Y F R F Q E E	795
2386	ATA AAA GAA AAC ACA AAG AAC GAC AAA CAA ATG GTC CAA TAT ATT	2430
796	I K E N T K N D K Q M V Q Y I	810

36/41

Continuation of Figure 25

2431	TAC	AAA	TAC	ACA	AGT	TAT	CCT	GAC	CCT	ATA	TTG	TTG	ATG	AAA	AGT	2475
811	Y	K	Y	T	S	Y	P	D	P	I	L	L	M	K	S	825
2476	GCT	AGA	AAT	AGT	TGT	TGG	TCT	AAA	GAT	GCA	GAA	TAT	GGA	CTC	TAT	2520
826	A	R	N	S	C	W	S	K	D	A	E	Y	G	L	Y	840
2521	TCC	ATC	TAT	CAA	GGG	GGA	ATA	TTT	GAG	CTT	AAG	GAA	AAT	GAC	AGA	2565
841	S	I	Y	Q	G	G	I	F	E	L	K	E	N	D	R	855
2566	ATT	TTT	GTT	TCT	GTA	ACA	AAT	GAG	CAC	TTG	ATA	GAC	ATG	GAC	CAT	2610
856	I	F	V	S	V	T	N	E	H	L	I	D	M	D	H	870
2611	GAA	GCC	AGT	TTT	TTC	GGG	GCC	TTT	TTA	GTT	GGC	TGA				2646
871	E	A	S	F	F	G	A	F	L	V	G	*				881

37/41

Figure 26

Nucleic acid sequence and corresponding amino acid sequence of scTNF-AMAIZE**Construct H**

1	ATG	GAC	TGG	ACC	TGG	CGC	GTG	TTT	TGC	CTG	CTC	GCC	GTG	GCT	CCT	45
1	M	D	W	T	W	R	V	F	C	L	L	A	V	A	P	15
46	GGG	GCC	CAC	AGC	CAG	GTA	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGC	ATG	90
16	G	A	H	S	Q	V	Q	L	V	Q	S	G	G	G	M	30
91	GTA	GAG	CCT	GGG	GGG	TCC	CTT	AGA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	135
31	V	E	P	G	G	S	L	R	L	S	C	A	A	S	G	45
136	TTC	ACT	TTC	AGT	AAT	GCC	TGG	ATG	AGC	TGG	GTC	CGC	CAG	GCT	CCA	180
46	F	T	F	S	N	A	W	M	S	W	V	R	Q	A	P	60
181	GGG	AAG	GGG	CTG	GAG	TGG	GTT	GGC	CGT	ATA	AAA	AGC	AAA	GCT	GGT	225
61	G	K	G	L	E	W	V	G	R	I	K	S	K	A	G	75
226	GGT	GGG	ACA	GCA	GAG	TAC	GCT	GCA	CCC	GTG	AAA	GGC	AGA	TTC	ACC	270
76	G	G	T	A	E	Y	A	A	P	V	K	G	R	F	T	90
271	ATC	TCA	AGA	GAT	GAT	TCA	CAA	AAC	ACG	CTG	TAT	CTG	CAA	ATG	AAC	315
91	I	S	R	D	D	S	Q	N	T	L	Y	L	Q	M	N	105
316	AGC	CTG	AAA	ACC	GAC	GAC	ACA	GCC	GTG	TAT	TAC	TGT	ACC	ACA	CAT	360
106	S	L	K	T	D	D	T	A	V	Y	Y	C	T	T	H	120
361	GTC	TAC	GGT	GCC	CCC	CGG	AAC	TGG	GGC	CAG	GGA	TCC	CTG	GTC	ACC	405
121	V	Y	G	A	P	R	N	W	G	Q	G	S	L	V	T	135
406	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	AAG	CTT	GAA	GAA	GGT	GAA	450
136	V	S	S	A	S	T	K	G	P	K	L	E	E	G	E	150
451	TTT	TCA	GAA	GCA	CGC	GTA	CAG	TCT	GTG	TTG	ACT	CAG	CCG	CCC	TCA	495
151	F	S	E	A	R	V	Q	S	V	L	T	Q	P	P	S	165
496	GTG	TCT	GCG	GCC	CCA	GGA	CAG	AAG	GTC	ACC	ATC	TCC	TGC	TCT	GGA	540
166	V	S	A	A	P	G	Q	K	V	T	I	S	C	S	G	180
541	AGC	AGC	TCC	AAC	ATT	GGA	AAT	AAT	TAT	GTC	TCC	TGG	TAC	GTT	CAA	585
181	S	S	S	N	I	G	N	N	Y	V	S	W	Y	V	Q	195
586	CTC	CCA	GGA	ACA	GCC	CCC	AAA	CTC	CTC	ATT	TAT	GAC	AAT	AAT	AAG	630
196	L	P	G	T	A	P	K	L	L	I	Y	D	N	N	K	210
631	CGA	TTC	TCA	GGA	GTT	CCT	GAC	CGA	TTC	TCT	GGC	TCC	AAG	TCT	GGC	675
211	R	F	S	G	V	P	D	R	F	S	G	S	K	S	G	225
676	ACG	TCA	GCC	ACC	CTG	GGC	ATC	ACC	GGG	CTC	CAG	ACT	GGG	GAC	GAG	720
226	T	S	A	T	L	G	I	T	G	L	Q	T	G	D	E	240
721	GCC	GAT	TAT	TAC	TGC	GGA	GCA	TGG	GAT	GGC	AGC	CTG	CGT	GAA	GCG	765
241	A	D	Y	Y	C	G	A	W	D	G	S	L	R	E	A	255

38/41

Continuation of Figure 26

766	GTA	TTC	GGC	GGA	GGG	ACC	AAG	GTC	ACC	GTC	CTA	GGT	GCG	GCC	GCA	810
256	V	F	G	G	G	T	K	V	T	V	L	G	A	A	A	270
811	GTT	GAG	CTC	GAG	GCG	GCC	GCG	GAT	TAC	AAA	GAC	GAT	GAC	GAT	AAA	855
271	V	E	L	E	A	A	A	D	Y	K	D	D	D	D	K	285
856	GAA	TTC	GGA	TCA	TCT	TCT	CGA	ACC	CCG	AGT	GAC	AAG	CCT	GTA	GCC	900
286	E	F	G	S	S	S	R	T	P	S	D	K	P	V	A	300
901	CAT	GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	GGG	CAG	CTC	CAG	TGG	CTG	945
301	H	V	V	A	N	P	Q	A	E	G	Q	L	Q	W	L	315
946	AAC	CGC	CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	990
316	N	R	R	A	N	A	L	L	A	N	G	V	E	L	R	330
991	GAT	AAC	CAG	CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	1035
331	D	N	Q	L	V	V	P	S	E	G	L	Y	L	I	Y	345
1036	TCC	CAG	GTC	CTC	TTC	AAG	GGC	CAA	GGC	TGC	CCC	TCC	ACC	CAT	GTG	1080
346	S	Q	V	L	F	K	G	Q	G	C	P	S	T	H	V	360
1081	CTC	CTC	ACC	CAC	ACC	ATC	AGC	CGC	ATC	GCC	GTC	TCC	TAC	CAG	ACC	1125
361	L	L	T	H	T	I	S	R	I	A	V	S	Y	Q	T	375
1126	AAG	GTC	AAC	CTC	CTC	TCT	GCC	ATC	AAG	AGC	CCC	TGC	CAG	AGG	GAG	1170
376	K	V	N	L	L	S	A	I	K	S	P	C	Q	R	E	390
1171	ACC	CCA	GAG	GGG	GCT	GAG	GCC	AAG	CCC	TGG	TAT	GAG	CCC	ATC	TAT	1215
391	T	P	E	G	A	E	A	K	P	W	Y	E	P	I	Y	405
1216	CTG	GGA	GGG	GTC	TTC	CAG	CTG	GAG	AAG	GGT	GAC	CGA	CTC	AGC	GCT	1260
406	L	G	G	V	F	Q	L	E	K	G	D	R	L	S	A	420
1261	GAG	ATC	AAT	CGG	CCC	GAC	TAT	CTC	GAC	TTT	GCC	GAG	TCT	GGG	CAG	1305
421	E	I	N	R	P	D	Y	L	D	F	A	E	S	G	Q	435
1306	GTC	TAC	TTT	GGG	ATC	ATT	GCC	CTG	GGT	GGC	GGT	TCT	GGT	GGC	GGT	1350
436	V	Y	F	G	I	I	A	L	G	G	G	S	G	G	G	450
1351	TCT	GGT	GGC	GGT	TCT	GGT	GGC	GGA	TCA	TCA	TCT	TCT	CGA	ACC	CCG	1395
451	S	G	G	G	S	G	G	G	S	S	S	S	R	T	P	465
1396	AGT	GAC	AAG	CCT	GTA	GCC	CAT	GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	1440
466	S	D	K	P	V	A	H	V	V	A	N	P	Q	A	E	480
1441	GGG	CAG	CTC	CAG	TGG	CTG	AAC	CGC	CGG	GCC	AAT	GCC	CTC	CTG	GCC	1485
481	G	Q	L	Q	W	L	N	R	R	A	N	A	L	L	A	495
1486	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	CTG	GTG	GTG	CCA	TCA	GAG	1530
496	N	G	V	E	L	R	D	N	Q	L	V	V	P	S	E	510
1531	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	TTC	AAG	GGC	CAA	GGC	1575
511	G	L	Y	L	I	Y	S	Q	V	L	F	K	G	Q	G	525
1576	TGC	CCC	TCC	ACC	CAT	GTG	CTC	CTC	ACC	CAC	ACC	ATC	AGC	CGC	ATC	1620
526	C	P	S	T	H	V	L	L	T	H	T	I	S	R	I	540

Continuation of Figure 26

[illegible]

40/41

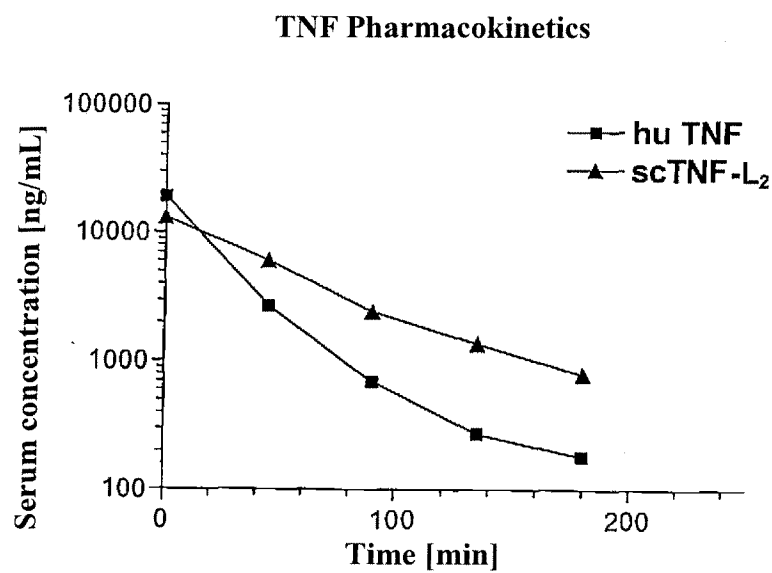


Figure 27

41/41

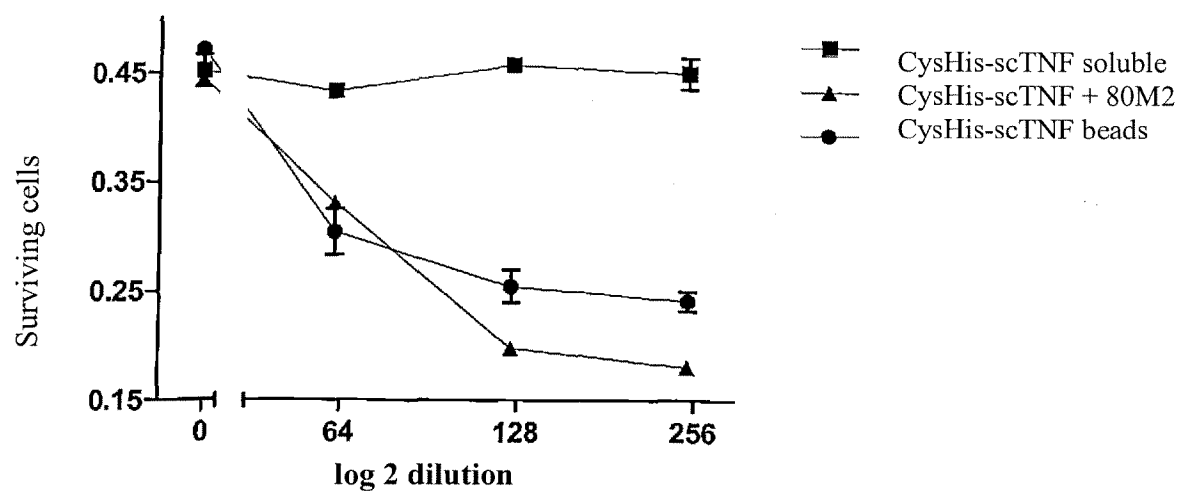


Figure 28